

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:19:49 ; Search time 7101 Seconds
(without alignments)

10860.525 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206
Sequence: 1 gfgccctcgaagcttccaagt.....aataaaccataactac 1206

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl: *
1: gb_env:*
2: gb_pat:*
3: gb_ph:*
4: gb_pl:*
5: gb_pr:*
6: gb_ro:*
7: gb_scs:*
8: gb_sy:*
9: gb_un:*
10: gb_vl:*
11: gb_ov:*
12: gb_hlg:*
13: gb_in:*
14: gb_cm:*
15: gb_da:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1206	100.0	1206	6	AF321553 Mus muscu
2	1200.4	99.5	1235	6	AY320031 Mus muscu
3	855	70.9	870	6	BC106776 Mus muscu
4	684	56.7	684	6	AF350409 Mus muscu
5	669.4	55.5	862	6	AY137338 Mus muscu
6	667.8	55.4	4263	6	AF320598 Mus muscu
7	667.8	55.4	197971	6	AC142191 Mus muscu
8	667.8	55.4	210200	6	AC157659 Mus muscu
9	629.2	52.2	2232	2	CQ086866 Sequence
10	624.4	51.8	984	6	AY137342 Mus muscu
11	624.4	51.8	1096	6	AY137341 Mus muscu
12	602	49.9	988	6	AF121352 Mus muscu
13	602	49.9	1014	6	AY137345 Mus muscu
14	601.8	49.9	933	6	AY256576 Mus muscu
15	601.4	49.9	1016	6	AY256575 Mus muscu
16	601.4	49.9	1026	6	AY137344 Mus muscu
17	601.4	49.9	1093	6	AY256574 Mus muscu
18	497.4	41.2	598	6	AB091366 Mus muscu

19	452.4	37.5	693	6	AF350411	AF350411 Mus muscu
20	364.4	30.2	1628	6	AF321552	AF321552 Rattus no
21	336.4	27.9	2127	6	BC051091	BC051091 Mus muscu
22	335.2	27.8	1464	6	BC086997	BC086997 Rattus no
23	318.4	26.4	1490	6	BC021766	BC021766 Mus muscu
24	316.6	26.3	797	6	AF350410	AF350410 Mus muscu
25	254.8	21.1	2714	6	AF320595	AF320595 Mus muscu
26	254.8	21.1	4679	6	AY137339	AY137339 Mus muscu
27	254.8	21.1	75164	2	CQ086895	CQ086895 Sequence
28	254.8	21.1	193034	6	AC174446	AC174446 Mus muscu
29	254.8	21.1	208074	12	AC153989	AC153989 Mus muscu
30	254.8	21.1	209064	6	AC159305	AC159305 Mus muscu
31	249.6	20.7	191955	6	AC102693	AC102693 Mus muscu
32	249.6	20.7	208074	12	AC153989	AC153989 Mus muscu
33	233.6	19.4	835	5	AY084051	AY084051 Homo sapi
34	213	17.7	9546	6	AY137343	AY137343 Mus muscu
35	204.4	16.9	62919	12	AC099883	AC099883 Mus muscu
36	179.2	14.9	230611	12	AC126655	AC126655 Rattus no
37	176	14.6	250	2	BD223286	BD223286 Toxicolog
38	169	14.0	168117	6	AC132352	AC132352 Mus muscu
39	169	14.0	231239	12	AC133164	AC133164 Mus muscu
40	167.4	13.9	9450	6	AF320596	AF320596 Mus muscu
41	167.4	13.9	303656	12	AC025528	AC025528 Mus muscu
42	145	12.0	166259	10	AY689436	AY689436 Deerpox v
43	143.8	11.9	823	5	AF285087	AF285087 Homo sapi
44	143.8	11.9	843	2	CQ727163	CQ727163 Sequence
45	143.8	11.9	850	2	CS034009	CS034009 Sequence

ALIGNMENTS

RESULT 1
AF321553 1206 bp mRNA linear ROD 07-MAY-2001
LOCUS Mus musculus osteoclast inhibitory lectin (Occl) mRNA, complete
DEFINITION

AF321553
AF321553 GI:13958627
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM

REFERENCE
AUTHORS Zhou,H., Kartsoiannidis,V., Hu,Y.S., Elliott,J., Quinn,J.M.,
1 (bases 1 to 1206)
1 (bases 1 to 1206)

TITLE
A novel osteoblast-derived C-type lectin that inhibits osteoclast
formation

JOURNAL J. Biol. Chem. 276 (18), 14916-14923 (2001)
PUBMED 11278931
2 (bases 1 to 1206)
AUTHORS Zhou,H.

TITLE Direct Submission
JOURNAL Submitted (15-NOV-2000) Department of Medicine, St. Vincent's
Hospital, The University of Melbourne, 41 Victoria Parade, Fitzroy,
Victoria 3065, Australia

FEATURES
source location/Qualifiers

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ORIGIN

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 IPIRBERPARYLNNGISSTRYISLRMMICSLNYSILHCOTPPFPS"

Query Match 100.0%; Score 1206; DB 6; Length 1206;
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 Matches 1206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTCTGAGCTTTCAAGTTTCAATCTGTAAGTGAAGAACTCAGCTCTCAGCTGAGA 60
 1 GTGCTCTGAGCTTTCAAGTTTCAATCTGTAAGTGAAGAACTCAGCTCTCAGCTGAGA 60
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 61 TGTGTCTCAAGAAAGGTTCCCTACCTATAGTCCCAAGGACCCGACAGAGGTG 120
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 121 AAGTGGTAAATTTCTCAAGAAAGGACCGAAACAATCTCCCTGAGTCTTGTGCTA 180
 181 AGCTTACTGCTACTATGAGATGATATGCTCTCACTGAGCTGTAATTGCTTTCTG 240
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 361 GGAATCTGCGCCAGGCTCTGTCATGACGACAGAGGCCCACTAGCTCGTTTGACAACC 420
 421 AGAATAGCTGAATTTCTTAATAGATACAGAGCAATTTGATTCCTGATGGCTGC 480
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 541 TTCCCATCCGGGAGAGAAAGATTGCTTACCTGAACAACAACGGGATCAGCAGTACCA 600
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 781 AACATGAGAAATGAAAAACATCAATTCATTTCAATGACAGAAATGTTCAAGTGTAAATC 840
 841 ACTGACTACTCTTCCGAGAGTCTGAGTTCATCTGAGCAACACATGCTGCTCAAA 900
 841 ACTGACTACTCTTCCGAGAGTCTGAGTTCATCTGAGCAACACATGCTGCTCAAA 900
 901 ACATCCGTAATGAGATCTTCTGAGGTATGAAAAACGCTACACTGTATTAATCTCTG 960
 901 ACATCCGTAATGAGATCTTCTGAGGTATGAAAAACGCTACACTGTATTAATCTCTG 960

QY 961 CAATTTAAAGCATGAGGAGCATAGAGATTAGTACCACCACTGATAGTCCCAAAA 1020
 DB 961 CAATTTAAAGCATGAGGAGCATAGAGATTAGTACCACCACTGATAGTCCCAAAA 1020
 QY 1021 GGACGAAATACAGGCTAAAGAAAGCTCTTGAACCTCTTCAATCTTCTCTCTCTG 1080
 DB 1021 GGACGAAATACAGGCTAAAGAAAGCTCTTGAACCTCTTCAATCTTCTCTCTCTG 1080
 QY 1081 GTCTTTTAAACACCAAGTCTGAGAGAAAGATGAGAAATGGGGAGGAGGAGG 1140
 DB 1081 GTCTTTTAAACACCAAGTCTGAGAGAAAGATGAGAAATGGGGAGGAGGAGG 1140
 QY 1141 GAGAGGACATGATTGGGGAGGAGGAGGAGGAGGAAATTAATTAATAAACCANA 1200
 DB 1141 GAGAGGACATGATTGGGGAGGAGGAGGAGGAGGAGGAAATTAATTAATAAACCANA 1200
 QY 1201 TACTAC 1206
 DB 1201 TACTAC 1206

RESULT 2
 AY320031 1235 bp mRNA linear ROD 10-MAR-2004
 LOCUS AY320031
 DEFINITION Mus musculus osteoclast inhibitory lectin (Oc11) mRNA, complete cds.
 ACCESSION AY320031
 VERSION AY320031.1 GI:33356564
 KEYWORDS
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE
 AUTHORS Carlyle,J.R., Jamieson,A.M., Gasser,S., Clingan,C.S., Arase,H. and Raulat,D.H.
 TITLE Missing self-recognition of Oc11/Clr-b by inhibitory NKR-P1 natural killer cell receptors
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101 (10), 3527-3532 (2004)
 PUBMED 14990792

REFERENCE
 AUTHORS Carlyle,J.R., Jamieson,A.M., Gasser,S., Clingan,C.S., Arase,H. and Raulat,D.H.
 TITLE Direct Submission
 JOURNAL Submitted (10-0UN-2003) Molecular & Cell Biology, University of California Berkeley, 485 Life Sciences Addition #3200, Berkeley, CA 94720-3200, USA

FEATURES
 source
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 Location/Qualifiers

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 /db_xref="taxon:10090"
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 1..66
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 67..690
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5' UTR

CDS

/note="C-type lectin related-B; type II transmembrane lectin-like protein"
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 /protein_id="AA016529.1"
 /db_xref="GI:33356565"
 /translation="MCTVKASH.PMLSPGSPGSEVVEVKKILOGRKHGTIIPESCAKLYC"

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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:19:57 ; Search time 5491 Seconds

(without alignments)
12281.682 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206
Sequence: 1 gggccctcagcttcaagt.....aaataaaccataactac 1206

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est3:*
3: gb_est4:*
4: gb_est5:*
5: gb_est6:*
6: gb_est7:*
7: gb_est8:*
8: gb_est9:*
9: gb_est10:*
10: gb_est11:*
11: gb_est12:*
12: gb_est13:*
13: gb_est14:*
14: gb_est15:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	627.6	52.0	2232	6	AK014570	AK014570 Mus muscu
2	627.6	52.0	2403	6	AK137753	AK137753 Mus muscu
3	602	49.9	2764	6	AK041724	AK041724 Mus muscu
4	502	41.6	969	6	BY714008	BY714008 BY714008
5	449.4	37.3	477	7	BF454103	BF454103 maasBp09.
6	446.4	37.0	468	7	AM113425	AM113425 MC1988 mo
7	439.8	36.5	605	4	CB581560	CB581560 ANGNNTC:N
8	432.4	35.9	424	7	BF660971	BF660971 maasBp09.
9	431.4	35.8	444	1	AI180635	AI180635 uc67109.t
10	424	35.2	424	1	BF453698	BF453698 maasBp09.
11	421.2	34.9	448	7	AM113424	AM113424 MC1988 mo
12	407.8	33.8	926	7	BF182123	BF182123 601804663
13	394	32.7	394	2	BG091810	BG091810 mac17604.
14	391.8	32.5	389	1	AA177493	AA177493 mc15c09.t
15	372	30.8	658	4	BY723071	BY723071 BY723071
16	370	30.7	394	1	AA797274	AA797274 vv23e07.t
17	365.8	30.3	401	2	BG230151	BG230151 mac28d03.
18	365	30.3	376	1	AA218025	AA218025 mv59f08.t
19	362	30.0	362	7	BF146984	BF146984 uw72d04.y

20	358	29.7	391	1	AA797334	AA797334 vv23g07.t
21	348.4	28.9	352	7	AW987086	AW987086 uf13h04.x
22	338	28.0	338	1	AI786472	AI786472 uf13h04.y
23	336.4	27.9	894	3	BUS23257	BUS23257 AGENCOURT
24	318.4	26.4	2158	6	AK090364	AK090364 Mus muscu
25	310.4	25.7	560	3	BQ264893	BQ264893 NISC ff02
26	309.8	25.7	976	3	BQ935069	BQ935069 AGENCOURT
27	308	25.5	1212	6	AK017207	AK017207 Mus muscu
28	304.4	25.2	317	1	AA472200	AA472200 v998e12.t
29	298.2	24.7	688	4	BY733654	BY733654 BY733654
30	285	23.6	285	2	BG095407	BG095407 mac28d03.
31	278.6	23.1	848	10	DV728509	DV728509 RYL21153
32	275.4	22.8	304	1	AA172733	AA172733 mc06c10.t
33	273	22.6	673	4	BY716938	BY716938 BY716938
34	258.2	21.4	858	4	CA468141	CA468141 AGENCOURT
35	254.6	21.1	508	1	AI641897	AI641897 vq47h05.y
36	251	20.8	534	1	AI504668	AI504668 vq33d10.x
37	248.2	20.6	691	5	CK843446	CK843446 ui-R-B32-
38	239.2	19.8	926	2	BF783690	BF783690 602109488
39	236.4	19.6	428	1	AA871981	AA871981 vq47h05.t
40	233.2	19.3	572	4	BX520363	BX520363 BX520363
41	232.6	19.3	853	7	AM107057	AM107057 ui92d06.y
42	223.2	18.5	503	7	BF407755	BF407755 ui-R-B32-
43	216.2	17.9	509	1	AI230483	AI230483 EST227178
44	216.2	17.9	531	4	CB718857	CB718857 AKGNNTC:U
45	211.8	17.6	699	10	DV227774	DV227774 EST-AK161

ALIGNMENTS

RESULT 1	AK014570	2232 bp	mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632413B12 product:C LECTIN-RELATED PROTEIN C homolog (Mus musculus), full insert sequence.
LOCUS	AK014570		
DEFINITION	AK014570.1	GI:12852505	
ACCESSION	AK014570		
VERSION	AK014570.1		
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
1	Carninci, P. and Hayashizaki, Y.		
2	High-efficiency full-length cDNA cloning		
3	Meth. Enzymol. 303, 19-44 (1999)		
4	10349636		
REFERENCE			
1	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
2	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
3	Genome Res. 10 (10), 1617-1630 (2000)		
4	11042159		
TITLE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujisawa, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, D., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
JOURNAL	RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer		
PUBMED	Genome Res. 10 (11), 1757-1771 (2000)		
AUTHORS	Genome Res. 10 (11), 1757-1771 (2000)		
11076861			
4	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		
TITLE	Functional annotation of a full-length mouse cDNA collection		

JOURNAL Nature 409, 685-690 (2001)

REFERENCE The FANTOM Consortium, the RIKEN Genome Exploration Research Group

AUTHORS Phase I and II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS RIKEN Genome Exploration Research Group, Genome Science Group (Genome Network Core Team) and the FANTOM Consortium.

TITLE Antisense Transcription in the Mammalian Transcriptome

JOURNAL Science 309, 1564-1566 (2005)

REFERENCE 7

AUTHORS The FANTOM Consortium, Riken Genome Exploration Research Group and Genome Science Group (Genome Network Project Core Group).

TITLE The Transcriptional Landscape of the Mammalian Genome

JOURNAL Science 309, 1559-1563 (2005)

REFERENCE 8 (bases 1 to 2232)

AUTHORS Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hirooka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Komori, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submision

JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: genome-res@gs.c.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

FEATURES

source location/Qualifiers

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/tissue_type="skin"

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/dev_stage="0 day neonate"

38..847

/note="unnamed protein product; C LECTIN-RELATED PROTEIN C homolog [Mus musculus] (SPR1AAL7197, evidence: FASTY, 85.1%ID, 100%length, match=603)

putative"

/codon_start=1

/protein_id="BAB29435.1"

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ORIGIN

Query Match 52.0%; Score 627.6; DB 6; Length 2232;

Best Local Similarity 88.1%; Pred. No. 5,2e-164; Matches 725; Conservative 0; Mismatches 79; Indels 20; Gaps 4;

QY 128 TAAATATTCACAGAGAAAAGGACAGGAACCATCTCCCTGAGTCTGTGCTAAGCTTAA 187

DB 295 TAAATATTCACAGAGAAAAGGACAGGAACCATCTCCCTGAGTCTGTGCTAAGCTTAA 354

QY 188 CTGCTACTATGAGAGTGCATGATGATGCTCACTGATGCTGTAATGCTCTTCTGTTGCTT 247

DB 355 CTGCTGCTGTGAGAGTGCATGATGATGCTCACTGATGCTGTAATGCTCTTCTGTTGCTT 414

QY 248 GTACGACAAAGACAGAAACAGATCCAGTCAACAGACCTATGCTGCTTCCCGCAAAA 307

DB 415 GCACAGCAAAAGACAGAAACAGATCCATATCAACAAGACCTATGCTGCTGCGCCGAAAA 474

QY 308 CTGATTTGAGTGAATAAATGTTTTTATTTCTGAAATCCCAAGTAACGTGACATT 367

DB 475 CTGATTTGAGTGAATAAATGTTTTTATTTCTGAAATCCCAAGTAACGTGACATT 534

QY 368 CGCCACAGCCTTCTGATGAGCAACAAGAGCCCACTAGCTCGGTTGACAAACAGAGATGA 427

DB 535 CGCCACAGCCTTCTGATGAGCAACAAGAGCCCACTAGCTCGGTTGACAAACAGAGATGA 594

QY 428 GCTGAATTTCTTAATGATATACAGGCGAATTTGATTCCTGATTTGCCCTGCACAGAA 487

DB 595 GCTGAATTTCTTAATGATATACAGGCGAATTTGATTCCTGATTTGCCCTGCACAGAA 654

QY 488 GTCTGTAGAGCAACCTTGGAAAGTGGACAGAAACCTGATTAACAACAGATTCCTCAT 547

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QY 548 CCGGAGAGAGAAAGATTTGCTTACCTGACCTGAACAACAAGGATCAGAGTACAGATCTTA 607

DB 715 CCAAGGAGTGGAAACATGTGCTTACCTGACCGGCAATGGATATAGAGTTCCAGGACATTA 774

QY 608 TTCATTGAGATGTGATGTGATGCAAGCTCAACACCTATATGCTTCACTGCCAAATCTCC 667

DB 775 TATACCTGGATATATGATGTGATGCAAGCTTAAACAATATGATGCTTCACTGCCAAATCTCC 834

QY 668 TTTTTCCTTCTTCTTACCATTTTACCAAGAGACGTTTTTGGCCGTATCTGCGGGGCTTA 727

DB 835 --TGTTCTGTCTTACCATTTTACCAAGAGACGTTTTTGGCCGTATCTGCGGGGCTTA 891

QY 728 CTCTTCCCTTATGATGCTTCCCAAGTGTATCAACACGATAGAGATATTTCTTAATCATCA 787

DB 892 CTCTTCCCTTATGATGCTTCCCAAGTGTATCAACACGATAGAGATATTTCTTAATCATCA 951

QY 788 GAAATGAAAACCATCATTTTCATTTTCATGCAAGATTTGTCAGTGTAAATCATCTGACT 847

DB 952 CAATGAAAACCATCATTTTCATTTTCATGCAAGATTTGTCAGTGTAAATCATCTGACT 1004

QY 848 ACTCTTCCGAAGTCTGTGATTCACATCTGAGCAACACATGCTGCTACAAACATCCG 907

DB 1005 GCTCTTCTGATGTCCGAGTTTACATCTGAGCAACACATGCTGCTTCTTAACAACATCTG 1064

QY 908 TAATGAGA-----TCTTCTGAGTGTATGAAGAAGCTACTACTT 951

DB 1065 TAATGACATCTTATGCTCTTCTGAGTGTGTGAAGAAACGCTACCTATCACT 1118

RESULT 2 AK137753

LOCUS AK137753

DEFINITION Mus musculus 6 days neonate skin cDNA, RIKEN full-length enriched library, clone: A030010M19 product: osteoclast inhibitory lectin related protein, full insert sequence.

ACCESSION AK137753

VERSION AK137753.1 GI:74202184

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:45:02 ; Search time 269 Seconds
(without alignments)
8388.689 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206
Sequence: 1 ggcgcctcgcgttcacgt.....aataaaccacaaatactac 1206

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 140366 seqs, 93554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: /EMC_Celerra_SIDS3/prodata/2/ina/6A_COMB.seq:*
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- 5: /EMC_Celerra_SIDS3/prodata/2/ina/7_COMB.seq:*
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- 9: /EMC_Celerra_SIDS3/prodata/2/ina/7_COMB.seq:*
- 10: /EMC_Celerra_SIDS3/prodata/2/ina/7_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	143.8	11.9	843	3	US-09-949-016-4429 Sequence 4429, Ap
2	142.8	11.8	573	3	US-09-531-056A-5 Sequence 5, Appl
3	102	8.5	519	3	US-09-531-056A-3 Sequence 3, Appl
4	102	8.5	582	3	US-09-531-056A-1 Sequence 1, Appl
5	102	8.5	931	3	US-09-531-056A-9 Sequence 9, Appl
6	93.4	7.7	90050	3	US-09-245-041-5 Sequence 5, Appl
7	93.4	7.7	90050	3	US-09-358-055B-5 Sequence 5, Appl
8	93.4	7.7	90050	3	US-09-358-055B-5 Sequence 5, Appl
9	92.8	7.7	44576	4	US-09-484-629B-17 Sequence 17, Appl
10	86.4	7.2	90050	3	US-09-245-041-5 Sequence 5, Appl
11	86.4	7.2	90050	3	US-09-358-055B-5 Sequence 5, Appl
12	86.4	7.2	90050	3	US-09-358-055B-5 Sequence 5, Appl
13	85.6	7.1	87874	3	US-09-893-238-5 Sequence 5, Appl
14	85.6	7.0	48974	3	US-08-920-422-17 Sequence 17, Appl
15	84.4	7.0	14707	3	US-09-312-762A-3 Sequence 3, Appl
16	83.6	6.9	759	3	US-09-944-807-5 Sequence 5, Appl
17	83.6	6.9	44576	4	US-09-484-629B-17 Sequence 17, Appl
18	81.6	6.8	13011	2	US-08-791-849A-14 Sequence 14, Appl
19	81.6	6.8	17056	3	US-09-245-041-5 Sequence 5, Appl
20	81.6	6.8	17056	3	US-09-358-055B-3 Sequence 3, Appl
21	81.6	6.8	17056	3	US-09-358-055B-3 Sequence 3, Appl
22	81.4	6.7	9196	3	US-09-971-773-3 Sequence 3, Appl
23	80.2	6.7	1652	3	US-10-199-945A-28 Sequence 28, Appl

C	24	79.2	6.6	1696	3	US-10-623-629-4	Sequence 4, Appl
C	25	78.6	6.5	5109	3	US-08-930-055A-2	Sequence 2, Appl
C	26	78.2	6.5	3205	3	US-09-061-768A-3	Sequence 3, Appl
C	27	78.2	6.5	3205	3	US-09-764-246-3	Sequence 3, Appl
C	28	77.4	6.4	1259	3	US-09-809-545A-40	Sequence 40, Appl
C	29	76.2	6.3	1422	3	US-09-784-642-6	Sequence 6, Appl
C	30	76.2	6.3	48974	3	US-08-920-422-17	Sequence 17, Appl
C	31	76	6.3	14507	3	US-08-785-150-1	Sequence 1, Appl
C	32	76	6.3	14507	3	US-09-660-299-1	Sequence 1, Appl
C	33	76	6.3	14507	3	US-09-435-377-1	Sequence 1, Appl
C	34	76	6.3	14507	3	US-09-973-928-1	Sequence 1, Appl
C	35	75.8	6.3	2801	3	US-09-869-588-27	Sequence 27, Appl
C	36	75.6	6.3	600	7	PCT-US93-10418-1	Sequence 1, Appl
C	37	75.6	6.3	1662	3	US-09-023-655-1241	Sequence 1, Appl
C	38	75.6	6.3	1676	3	US-09-949-016-4428	Sequence 4428, Ap
C	39	75.6	6.3	1702	3	US-09-023-655-1391	Sequence 1391, Ap
C	40	74.6	6.2	37950	3	US-09-949-016-258	Sequence 258, App
C	41	74.6	6.2	37950	3	US-09-338-907-183	Sequence 183, App
C	42	74.6	6.2	37950	3	US-09-218-207-183	Sequence 183, App
C	43	74.2	6.2	5039	3	US-09-386-816C-1	Sequence 1, Appl
C	44	74.2	6.2	5039	3	US-10-320-176-1	Sequence 1, Appl
C	45	73.4	6.1	35828	3	US-09-449-218D-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-4429
Sequence 4429, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTRI, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: C0001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4429
LENGTH: 843
TYPE: DNA
ORGANISM: Human
US-09-949-016-4429

Query Match 11.9%; Score 143.8; DB 3; Length 843;
Best Local Similarity 62.7%; Pred. No. 2.6e+35;
Matches 259; Conservative 0; Mismatches 147; Indels 7; Gaps 2;

289 ATGCTGCTGCGCCGCAAACTGATGAGTTGAAATAATGTTTATTTTTCGTAAT 348
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221 AAGCTGATGCGCCGCAAAAGCTGATTTGTTTCAAGAAAGTTTCTATTTTCGATG 280
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349 ACCCAAGTAACTGGAATTCGCCAGGCTTTCGATGCGACAAAGGCCCACTAGCTC 408
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281 ACACCAAGAACTGACATCAAGTCAAGGTTTGTGACTCACAAAGTGCATCTTGCTC 340
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409 GGTTCGACACCAAGATGAGTGAATTTCTTAATGATGACAAAGGCAATTTGATTCCT 468
|||||
341 AGGTTGAAGCTTCGAGAACTGAATTTCTGTTGATGATTAAGCCCATCTGATCACT 400
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469 GGATTGCTGCGCCGCAAGAGTGTCTGAGACACCTTGAAGTGTGACAGACCAACTGAGT 528
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401 GGATTGCTGCGCCGCAAGAGTGTCTGAGACACCTTGAAGTGTGACAGACCAACTGAGT 457
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529 ATTAACAACAGATTCCTCCATCCGGGAGAGAAAGATTTCCTTACCTGAACAAACGGGA 588
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Db 458 GGACAAAGACGTTTCTATCTCGGAGCAGAGAGTGCTATTTGAATGCAAAAGTGG 517
QY 589 TCAGCAGTACCGAGATCTTATCTTCGATGTGATCTGTAGCA---AGCTCAACAGC 644
Db 518 CCAAGTAGTCCAGGCACTACAGAGAGAGAGTGGATTTGTTCCAAATCAGATATACATG 577
QY 645 TATAGCTCCACGCGCAAACTCTTTTCTTCCCTAGCATTTTACCAGAGA 697
Db 578 TCTAGATGTTACGACAAAGCCCACTAATCTTTAGAGCATATTGGAACTGA 630

RESULT 2

US-09-531-056A-5
; Sequence 5, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-531-056A-5

Query Match 11.8%; Score 142.8; DB 3; Length 573;
Best Local Similarity 65.3%; Pred. No. 4,4e-35;
Matches 226; Conservative 0; Mismatches 117; Indels 3; Gaps 1;

QY 289 ATGCTGCTTCCCGCAAACTGAGTTGAGTTGAAAATAATGTTTATTTTCTGAT 348
Db 215 AAGCTCATGCCAGAAAGCTGATGTTTTCAAAAGAGTGTCTATTTTCTGATG 274
QY 349 ACCCAAGTACTGACATTTGCCAGGCTTCTGTCATGACACAAAGGCCCACTAGCTC 408
Db 275 ACACCAAGAACTGAGACATCAAGTCAGAGGTTTGTGCTACACAAAGTCTGATCTTGC 334
QY 409 GGTTCGACACCAAGATGAGTGAATTTCTTAATGATACAAAGGCCAATTTTGATTCCT 468
Db 335 AGCTTAAAGCTTCCAGGAATCTGAATTTCTGTGAGATATTAAGGCCCATCTGATCACT 394
QY 469 GGATTGGCTGCACAGAGTCTGTCAGAGCACCTTGGAGTGGACAGACAACTAGT 528
Db 395 GGAATGGGCTGACAGAGA---ACAAGGCCAACATGGAATGATGAATGTAATGTAAT 451
QY 529 ATTAACAACAGATTTCCCATTCGGGAGAGGAAAGATTTGCTTACCTGAACAACAGCGGA 588
Db 452 GGACAAAGACATTTCTATCTCTGAGAGCAGAGAGTGTGCTATTTGAAATGACAAAGTGT 511
QY 589 TCAGCAGTACAGAGATCTATTCATTCGATGTGATCTGTAGAGA 634
Db 512 CCAAGTAGTCCAGGCACTACACAGAGAGAGTGGATTTTTCGA 557

RESULT 3

US-09-531-056A-3
; Sequence 3, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3
; LENGTH: 519
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-531-056A-3

Query Match 8.5%; Score 102; DB 3; Length 519;
Best Local Similarity 63.7%; Pred. No. 5,2e-22;
Matches 172; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 289 ATGCTGCTTCCCGCAAACTGAGTTGAGTTGAAAATAATGTTTATTTTCTGAT 348
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QY 349 ACCCAAGTACTGACATTTGCCAGGCTTCTGTCATGACACAAAGGCCCACTAGCTC 408
Db 212 ACACCAAGAACTGAGACATCAAGTCTGAGTTTGTGACTACACAAAGTGTGATCTTGC 271
QY 409 GGTTCGACACCAAGATGAGTGAATTTCTTAATGATACAAAGGCCAATTTTGATTCCT 468
Db 272 AGCTTAAAGCTTCCAGGAATCTGAATTTCTGTGAGATATTAAGGCCCATCTGATCACT 331
QY 469 GGATTGGCTGCACAGAGTCTGTCAGAGCACCTTGGAGTGGACAGACAACTAGT 528
Db 332 GGAATGGGCTGACAGAGA---ACAAGGCCCAACATGGAATGATGAATGTAATGTAAT 388
QY 529 ATTAACAACAGATTTCCCATCCGCGGAGAG 558
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RESULT 4

US-09-531-056A-1
; Sequence 1, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-531-056A-1

Query Match 8.5%; Score 102; DB 3; Length 582;
Best Local Similarity 63.7%; Pred. No. 5,5e-22;
Matches 172; Conservative 0; Mismatches 95; Indels 3; Gaps 1;

QY 289 ATGCTGCTTCCCGCAAACTGAGTTGAGTTGAAAATAATGTTTATTTTCTGAT 348
Db 215 AAGCTCATGCCAGAAAGCTGATGTTTTCAAAAGAGTGTCTATTTTCTGATG 274
QY 349 ACCCAAGTACTGACATTTGCCAGGCTTCTGTCATGACACAAAGGCCCACTAGCTC 408
Db 275 ACACCAAGAACTGAGACATCAAGTCTGAGAGTGTGCTACACAAAGTCTGATCTTGC 334
QY 409 GGTTCGACACCAAGATGAGTGAATTTCTTAATGATACAAAGGCCAATTTTGATTCCT 468
Db 335 AGCTTAAAGCTTCCAGGAATCTGAATTTCTGTGAGATATTAAGGCCCATCTGATCACT 394
QY 469 GGATTGGCTGCACAGAGTCTGTCAGAGCACCTTGGAGTGGACAGACAACTAGT 528
Db 395 GGAATGGGCTGACAGAGA---ACAAGGCCAACATGGAATGATGAATGTAATGTAAT 451
QY 529 ATTAACAACAGATTTCCCATCCGCGGAGAG 558
Db 452 GGACAAAGACATTAATGATGAATGAAGAGATG 481

GenCore version 5.1.8
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	629.2	52.2	2232	9 US-10-388-838-12	Sequence 12, Appl
2	254.8	21.1	75164	9 US-10-388-838-11	Sequence 11, Appl
3	159.8	13.3	429	9 US-09-960-352-14614	Sequence 14614, A
4	144.4	12.0	1560	6 US-10-114-893-21	Sequence 21, Appl
5	144	11.9	2536	9 US-10-719-993-131	Sequence 136, App
6	144	11.9	2542	9 US-10-719-993-131	Sequence 131, App
7	144	11.9	2595	9 US-10-719-993-133	Sequence 133, App
8	144	11.9	2595	9 US-10-719-993-132	Sequence 132, App
9	144	11.9	2628	9 US-10-719-993-135	Sequence 135, App
10	143.8	11.9	850	7 US-10-335-009-5	Sequence 5, Appl
11	143.8	11.9	850	7 US-10-770-639-5	Sequence 5, Appl
12	143.8	11.9	850	12 US-10-501-841-28	Sequence 28, Appl
13	143.8	11.9	850	16 US-11-106-339-5	Sequence 5, Appl
14	143.8	11.9	2536	9 US-10-388-838-27	Sequence 27, Appl
15	143.8	11.9	2542	9 US-10-388-838-29	Sequence 29, Appl
16	143.8	11.9	2582	9 US-10-388-838-19	Sequence 19, Appl
17	143.8	11.9	2595	9 US-10-388-838-31	Sequence 31, Appl

18	143.8	11.9	2628	9	US-10-388-838-17	Sequence 17, Appl	
19	142.8	11.8	4450	10	US-10-775-204-2161	Sequence 2161, Appl	
20	106	8.8	203132	8	US-10-322-281-459	Sequence 459, App	
c	21	103	8.5	98638	11	US-10-330-773-896	Sequence 896, App
22	102.6	8.5	2162	3	US-09-822-846-169	Sequence 169, App	
23	102.6	8.5	2238	6	US-10-114-893-27	Sequence 27, Appl	
24	102.2	8.5	2706	9	US-10-719-993-130	Sequence 130, App	
25	102.2	8.5	2710	9	US-10-719-993-137	Sequence 137, App	
26	102	8.5	897	3	US-09-965-529-45	Sequence 45, Appl	
27	102	8.5	897	3	US-09-969-680A-45	Sequence 45, Appl	
28	102	8.5	897	13	US-11-048-692-45	Sequence 45, Appl	
29	102	8.5	1091	10	US-10-450-763-19609	Sequence 19609, A	
30	102	8.5	2706	9	US-10-388-838-15	Sequence 15, Appl	
31	102	8.5	2710	9	US-10-388-838-25	Sequence 25, Appl	
c	32	101.6	8.4	42514	6	US-10-087-192-475	Sequence 475, App
c	33	101.2	8.4	92969	11	US-10-330-773-178	Sequence 178, App
34	100	8.3	454	8	US-10-242-535A-43386	Sequence 43386, A	
35	100	8.3	454	8	US-10-085-783A-43386	Sequence 43386, A	
36	99.6	8.3	23611	8	US-10-322-281-61	Sequence 61, Appl	
c	37	98.6	8.2	50833	11	US-10-330-773-188	Sequence 188, App
c	38	98.6	8.2	59767	10	US-10-461-862-157	Sequence 157, App
c	39	97.8	8.1	236246	11	US-10-330-773-567	Sequence 567, App
40	97.6	8.1	78953	7	US-10-085-117-31	Sequence 31, Appl	
c	41	97.2	8.1	22281	6	US-10-087-192-1153	Sequence 1153, Ap
42	96.6	8.0	35159	6	US-10-087-192-91	Sequence 91, Appl	
c	43	96.2	8.0	5315	8	US-10-451-867A-1	Sequence 1, Appl
44	94.6	7.8	107432	11	US-10-330-773-137	Sequence 137, App	
45	94.2	7.8	38239	11	US-10-330-773-603	Sequence 603, App	

ALIGNMENTS

RESULT 1
US-10-388-838-12
; Sequence 12, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 2232
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-388-838-12

Query Match 52.2%; Score 629.2; DB 9; Length 2232;
Best Local Similarity 88.2%; Pred. No. 2.1e-185;
Matches 736; Conservative 0; Mismatches 78; Indels 20; Gaps 4;

QY	128	TAAATTTCTCCAGAAAAAGCAGCAACATCTCCCTGAGTCTTGCTAAGCTTTA	187
DB	295	TAAATTTCTCCAGAAAAAGCTCAGAGCACTCCCTGAGTCTTGCTAAGCTTTA	354
QY	188	CTGCTACTATGAGTATCATGTCTCTCACTAGCTGTATTTGCTTTGCTTT	247
DB	355	CTGCTCTATGAGTATCATGTCTCTCACTAGCTGTATTTGCTTTGCTTT	414
QY	248	GTCAGCAACAAAGACAGATCCAGTCAACAGAACTTATGCTTGCCGCAAAA	307
DB	415	GTCAGTAAACAAAGACAGATCTTATCAACAGAACTTATGCTTGCCGCAAAA	474
QY	308	CTGATTTGAGTGAATAATATTTATTTTCTGAATACCAAGTACGACATT	367
DB	475	CTGATTTGAGTGAATAATATTTATTTTCTGAATACCAAGTACGACATT	534
QY	368	CGCCAGGCGCTTGTGATGCGCAACAGGCCCACTAGCTCGTTTGACACAGATGA	427

GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 24, 2006, 20:05:24 ; Search time 849 Seconds

(without alignments)
9904.042 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 1206
Sequence: 1 gtcgccttcgccttcacgt.....aataaaccacaaatactac 1206

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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3: geneseqn2000s: *
4: geneseqn2001as: *
5: geneseqn2001bs: *
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13: geneseqn2004bs: *
14: geneseqn2005s: *
15: geneseqn2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1206	100.0	1206	4	AAFS8431	AAFS8431 Murine mo
2	711.4	59.0	713	4	AAFS8413	AAFS8413 Murine mo
3	669.4	55.5	862	4	AAFS8432	AAFS8432 Murine mo
4	629.6	52.2	990	4	AAFS8408	AAFS8408 Murine mo
5	629.2	52.2	2232	13	ADR67062	ADR67062 Mouse can
6	554	45.9	1907	4	AAFS8406	AAFS8406 Murine mo
7	500.4	41.5	633	4	AAFS8424	AAFS8424 Murine mo
8	493.4	40.9	721	4	AAFS8411	AAFS8411 Murine mo
9	386.2	32.0	620	4	AAFS8405	AAFS8405 Rat iOCiL
10	364.4	30.2	1628	4	AAFS8428	AAFS8428 Rat iOCiL
11	346.8	28.8	1302	4	AAFS8403	AAFS8403 Rat iOCiL
12	307	25.5	1907	4	AAFS8406	AAFS8406 Murine mo
13	277.6	23.0	738	4	AAFS8404	AAFS8404 Rat iOCiL
14	268.4	22.3	402	4	AAFS8400	AAFS8400 Rat iOCiL
15	254.8	21.1	9862	4	AAFS8407	AAFS8407 Murine can
16	176	14.6	75164	13	ADR67061	ADR67061 Mouse can
17	176	14.6	250	3	AAA10130	AAA10130 Rat liver
18	176	14.6	250	6	AAA42154	AAA42154 Rat target

19	159.8	13.3	429	8	ABX49449	ABX49449 Bovine ES
20	144.4	12.0	1305	4	AAFS8416	AAFS8416 Human hOC
21	144.4	12.0	1560	2	AAT91295	AAT91295 Human G52
22	144.4	12.0	1560	10	ADC38663	ADC38663 Human cDN
23	143.8	11.9	820	4	AAFS8436	AAFS8436 Human hOC
24	143.8	11.9	823	3	AAA28176	AAA28176 Human clo
25	143.8	11.9	845	4	AAFS8437	AAFS8437 Human hOC
26	143.8	11.9	850	10	ADDB67551	ADDB67551 Human Lyl
27	143.8	11.9	850	12	ADU93624	ADU93624 cDNA enco
28	143.8	11.9	850	12	ADP12837	ADP12837 Reference
29	143.8	11.9	850	12	ADO20148	ADO20148 Human PRO
30	143.8	11.9	850	13	ADRO6493	ADRO6493 Human LIL
31	143.8	11.9	850	14	ADY19967	ADY19967 DNA encod
32	143.8	11.9	850	14	ADY17709	ADY17709 DNA encod
33	143.8	11.9	850	15	AE811651	AE811651 Human lec
34	143.8	11.9	850	15	AE889843	AE889843 Human LIL
35	143.8	11.9	924	12	ADO21138	ADO21138 Human car
36	143.8	11.9	2353	7	ADR41233	ADR41233 Human CD-
37	143.8	11.9	2536	13	ADR67077	ADR67077 Human can
38	143.8	11.9	2542	13	ADR67079	ADR67079 Human can
39	143.8	11.9	2582	13	ADR67069	ADR67069 Human can
40	143.8	11.9	2595	13	ADR67081	ADR67081 Human can
41	143.8	11.9	2628	13	ADR67067	ADR67067 Human can
42	143.2	11.9	673	7	ADR41251	ADR41251 Human CD-
43	142.8	11.8	399	15	AER25547	AER25547 Human LIL
44	142.8	11.8	450	10	ADFI7039	ADFI7039 Human alb
45	142.8	11.8	576	15	AER25545	AER25545 Human lec

ALIGNMENTS

RESULT 1	AAFS8431	AAFS8431 standard; DNA; 1206 BP.
ID	AAFS8431	
XX	AAFS8431;	
AC	25-APR-2001 (first entry)	
XX		
DT		
XX		
DE	Murine mOCIL clone coding sequence.	
XX		
KW	Osteoparctic; mononuclear osteoclast precursor formation inhibition;	
KW	calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;	
KW	osteoclast differentiation; bone resorption; primary hyperparathyroidism;	
KW	Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;	
KW	humoral hypercalcaemia; cancer; ss.	
XX		
OS	Mus musculus.	
XX		
PN	MO200105964-A1.	
XX		
PD	25-JAN-2001.	
XX		
PF	19-JUL-2000; 2000MO-AU000864.	
XX		
PR	19-JUL-1999; 99AU-00001675.	
XX		
PA	(SVIN-) ST VINCENTS INST MEDICAL RES.	
PI	Zhou H, Kartsoyianis V, Hu Y, Gillespie MT, Ng KW;	
XX	WPI; 2001-103148/11.	
DR		
XX		
PT	Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed	
PT	on an osteoblast cell surface and used for treating excessive bone	
PT	resorption in conditions such as osteoporosis and Paget's disease.	
XX		
PS	Claim 4; Page 119; 131pp; English.	
XX		
CC	The present invention relates to osteoclast inhibitory lectin coding	
CC	sequences and proteins (OCIL). OCIL is a type II membrane protein which	
CC	is expressed on osteoblast cell surfaces. OCIL inhibits osteoclast	

CC differentiation from haematopoietic cell precursors. OCIL is useful for
 CC creating a condition with excessive bone resorption, including
 CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
 CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
 CC conditions where cancer has metastasised to the bone
 XX

Sequence 1206 BP; 356 A; 275 C; 267 G; 308 T; 0 U; 0 Other;

Query Match 100.0%; Score 1206; DB 4; Length 1206;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GTGCCCTCAGCTTCAAGTTTCAATCTGTAGTGAATACTCAGTCTCTCAGCTTGAGA 60
DB 1 GTGCCCTCAGCTTCAAGTTTCAATCTGTAGTGAATACTCAGTCTCTCAGCTTGAGA 60
QY 61 TGTGTGTCAAAAGGCTTCCCTAAGTGTAGTCCACAGGACGCGCAGAGGTAG 120
DB 61 TGTGTGTCAAAAGGCTTCCCTAAGTGTAGTCCACAGGACGCGCAGAGGTAG 120
QY 121 AAGTGGTAAATATTCCTCAAGGAAAGGACGGAACATCTCCCTGAGTCTTGTCGA 180
DB 121 AAGTGGTAAATATTCCTCAAGGAAAGGACGGAACATCTCCCTGAGTCTTGTCGA 180
QY 181 AGCTTACTGCTACTATGAGATGATGCTCCTCACTGAGCTGTAATTGCTTTCTG 240
DB 181 AGCTTACTGCTACTATGAGATGATGCTCCTCACTGAGCTGTAATTGCTTTCTG 240
QY 241 TTGCTTTGTGACGACAAAGACAAACAGATCCCAAGTCAACAAAGACTTATGCTTGCC 300
DB 241 TTGCTTTGTGACGACAAAGACAAACAGATCCCAAGTCAACAAAGACTTATGCTTGCC 300
QY 301 CGGAAACTGGAGTTGGAGTTGAAATTAATTTTATTTTCTGAAATACCAAGTAAT 360
DB 301 CGGAAACTGGAGTTGGAGTTGAAATTAATTTTATTTTCTGAAATACCAAGTAAT 360
QY 361 GGAATTCGCGCCAGGCTTGTGATGAGCAAGAGGCCCACTAGCTCGTTTGACAAAC 420
DB 361 GGAATTCGCGCCAGGCTTGTGATGAGCAAGAGGCCCACTAGCTCGTTTGACAAAC 420
QY 421 AGGATGAGCTGAATTTCTTAATGAGATACAAAGCGAATTTTGAATTCCTGAGTGGCTGC 480
DB 421 AGGATGAGCTGAATTTCTTAATGAGATACAAAGCGAATTTTGAATTCCTGAGTGGCTGC 480
QY 481 ACGAAGATGCTGAGACACCTTTGAAAGTGAACAGACACTGATTAACAAACGGA 540
DB 481 ACGAAGATGCTGAGACACCTTTGAAAGTGAACAGACACTGATTAACAAACGGA 540
QY 541 TTGCCATCCGGGAGAGGAAGATTGCTTACCTGAACAAACGAGGATCAGAGTACCA 600
DB 541 TTGCCATCCGGGAGAGGAAGATTGCTTACCTGAACAAACGAGGATCAGAGTACCA 600
QY 601 GGATCTAATTCATCTTGGATGTGATCTGAGCAAGCTCAACAGCTATAGCTCCACGTC 660
DB 601 GGATCTAATTCATCTTGGATGTGATCTGAGCAAGCTCAACAGCTATAGCTCCACGTC 660
QY 661 AAATCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
DB 661 AAATCTCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 720
QY 721 GGTGCTACTCTTCCCTATGATCCCAAGTGCATCAACAGATAGAGATATTTCTT 780
DB 721 GGTGCTACTCTTCCCTATGATCCCAAGTGCATCAACAGATAGAGATATTTCTT 780
QY 781 AACATAGAAATGAAACCAATCAATTTCAATTCATGACAGAGATTGTTCAAGTGTAAATC 840
DB 781 AACATAGAAATGAAACCAATCAATTTCAATTCATGACAGAGATTGTTCAAGTGTAAATC 840
QY 841 ACTGACTACTCTTCCGAGGCTGAGTTCATCTGAGCAACCAACATGAGTGTGCTCAAA 900
DB 841 ACTGACTACTCTTCCGAGGCTGAGTTCATCTGAGCAACCAACATGAGTGTGCTCAAA 900
QY 901 ACATCCGATATGAGATCTTCTGAGGTGTATGAAAAACAGTACATGTAATTAATCTCTG 960
  
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DB 901 ACATCCGATATGAGATCTTCTGAGGTGTATGAAAAACAGTACATGTAATTAATCTCTG 960
QY 961 CAATTTAAAGCATGAGGACATGAGAGATTGCTTACCCCACTGATAGTCCCAAAA 1020
DB 961 CAATTTAAAGCATGAGGACATGAGAGATTGCTTACCCCACTGATAGTCCCAAAA 1020
QY 1021 GGACGAAATATACAGGCTTAAAGACCTCTTGAACCTCTTCAATCTCTTCTCTCTG 1080
DB 1021 GGACGAAATATACAGGCTTAAAGACCTCTTGAACCTCTTCAATCTCTTCTCTCTG 1080
QY 1081 GTCTTTTAAAGACCAAGTCTGAGAGAAAGATGAGAAATGGGAAAGGAGG 1140
DB 1081 GTCTTTTAAAGACCAAGTCTGAGAGAAAGATGAGAAATGGGAAAGGAGG 1140
QY 1141 GAGAGGACATGATTGGGGGAGGGGAGGAGGAAATTAATTAATTAATTAATTAAT 1200
DB 1141 GAGAGGACATGATTGGGGGAGGGGAGGAGGAAATTAATTAATTAATTAATTAAT 1200
QY 1201 TACTAC 1206
DB 1201 TACTAC 1206
  
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RESULT 2
 AAF58413
 ID AAF58413 standard; DNA; 713 BP.

AAF58413;
 DT 25-APR-2001 (first entry)

XX Murine MOCIL17 clone coding sequence #1.

XX Osteopathic; mononuclear osteoclast precursor formation inhibition;
 XX calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;
 XX osteoclast differentiation; bone resorption; primary hyperparathyroidism;
 XX Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;
 XX humoral hypercalcaemia; cancer; ss.

XX Mus musculus.
 OS
 PN W0200105964-A1.

PD 25-JAN-2001.

XX 19-JUL-2000; 2000MO-AU000864.

XX 19-JUL-1999; 99AU-00001675.

XX (SVIN-) ST VINCENTS INST MEDICAL RES.

XX Zhou H, Kartsojiannis V, Hu Y, Gillespie MT, Ng KW;

XX WPI; 2001-103148/11.

XX Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed
 PT on an osteoclast cell surface and used for treating excessive bone
 PT resorption in conditions such as osteoporosis and Paget's disease.

XX Example 11; Page 109; 131p; English.

XX The present invention relates to osteoclast inhibitory lectin coding
 CC sequences and proteins (OCIL). OCIL is a type II membrane protein which
 CC is expressed on osteoclast cell surfaces. OCIL inhibits osteoclast
 CC differentiation from haematopoietic cell precursors. OCIL is useful for
 CC treating a condition with excessive bone resorption, including
 CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
 CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
 CC conditions where cancer has metastasised to the bone

XX Sequence 713 BP; 190 A; 179 C; 157 G; 187 T; 0 U; 0 Other;

Oy	469	GGATTGGGCTGCA	CAGAGAGTGTG	TAGBACAC	CCCTTGGAA	AGTGGAC	AGACAC	AACCTGAG	528
Db	408	GGATTGGGCTG	GACAGAG	---ACAAGG	CCACCAATG	GAATGGA	TAATGTG	TACTGAAAT	464
Oy	529	ATTAACAACAGAT	TTTCCATCCG	GGGGAGAGAA	AGATTGCTCA	CTGAACA	CAACAGGGA	588	
Db	465	GGACAAGACAGT	TTTCTTATCT	CTGGAGAC	AGAGTGTG	CTATTTG	GAATGACAA	AGGTG	524
Oy	589	TCAGCAGTAC	CAGATCTAT	TTCACCTT	CGAGTGTG	ATCTGTACA	---AGTCA	ACAGC	644
Db	525	CCAGTAGTGCC	AGGACACT	CACAGAGAG	GAAGTGGA	TTGTTCCAA	TATCAGATAT	CAATG	584
Oy	645	TATACCTCCAC	TGCGAACT	CTCTTTTTC	TCTCCTAG	ATTTACCA	AGAGA	697	
Db	585	TCTATATGTTA	CAGCAAG	CCCCCACT	TAATCTTT	TGAAGATAT	GTGAAC	TGA	637

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RESULT 2
US-10-488-619-1138/C
; Sequence 1138, Application US/10488619
; Publication No. US2006009578A1
; GENERAL INFORMATION:
; APPLICANT: Greentree, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488, 619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1138
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1138

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Query Match	6.3%	Score 76.4;	DB 6;	Length 553;
Best Local Similarity	75.7%;	Pred. No. 11e-13;		
Matches 112; Conservative	0;	Mismatches 26;	Indels 10;	Gaps 11.

QY	814	TCACAGATTTGTTCAAGTGGTTAAATCACTGACTACTCTTCCGAAGGTCTTGAGTTCA	873
Db	175	TGGCAAGACGGCTCCAGCAGTAAGACACTGACTCTTCTTCCAAAGGCTTGAGTTCAAA	116
QY	874	TCTGAGCAACCACTGCTGGCTCACAAACATCCGTAATAGA-----TCTTTCTGA	923
Db	115	TCCCAACAACCACTGCTGGCTCACAAACCATATGATCTGACGCGCTTCTTCTGG	56
QY	924	GGTGATATGAAAACAGCTACACTGTACTT	951
Db	55	TATGTCTGAAGACAGCTACAGTACTT	28

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RESULT 3
US-10-488-619-1139
; Sequence 1139, Application US/10488619
; Publication No. US20060099578A1
; GENERAL INFORMATION:
; APPLICANT: Greentree, Winner and Sullivan, P.C.
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations
; TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays
; FILE REFERENCE: 98-01 WO
; CURRENT APPLICATION NUMBER: US/10/488,619
; CURRENT FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 3040
; SOFTWARE: Patcentin version 3.1
; SEQ ID NO 1139
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-488-619-1139

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Query Match 6.3%; Score 76.4; DB 6; Length 577;

	Best Local Similarity 75.7%; Pred. No. 1,1e-13; Matches 112; Conservative 0; Mismatches 26; Indels 10; Gaps 1
QY	814 TGCAGAGATTGTTCAAGTGTAAATAATCACTGACTCTTTCCGAAGGTCCTGAGTTTACA 873
Db	424 TGGCAGACGGCTCAGCAGGTAAAGCAGCTACGTGTTCTTCAAAAGGTCCTGAGTTTCAA 483
QY	874 TCTGAGCAACACATGAGTGCTCAACAAATCCGTATGAGA-----TCTTCTGA 923
Db	484 TCCAGCAACCAATGAGTGCTCAACCAACCATATATGAGATGTGACGCGCTTCTTCTGG 543
QY	924 GGTGTATGAAACAGCTACTGATCTT 951
Db	544 TATGTCTGAAACAGCTACAGTGAATT 571

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/ RESULT 4
/ US-10-511-937-429
/ Sequence 429, Application US/10511937
/ Publication No. US2006008836a1
/ GENERAL INFORMATION:
/ APPLICANT: EXPRESSION DIAGNOSTICS, INC.
/ APPLICANT: Wohlgenuth, Jay
/ APPLICANT: Fry, Kirk
/ APPLICANT: Woodward, Robert
/ APPLICANT: Ly, Ngoc
/ APPLICANT: Prentice, James
/ APPLICANT: Morris, Macdonald
/ APPLICANT: Rosenberg, Steven
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
/ TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
/ FILE REFERENCE: 506612000104
/ CURRENT APPLICATION NUMBER: US/10/511,937
/ CURRENT FILING DATE: 2004-10-19
/ PRIOR APPLICATION NUMBER: PCT/US2003/012946
/ PRIOR FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 10/131,831
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 10/325,899
/ PRIOR FILING DATE: 2002-12-20
/ NUMBER OF SEQ ID NOS: 3117
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO: 429
/ LENGTH: 1702
/
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-511-937-429

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Query Match	6.3%	Score 75.6;	DB 6;	Length 1702;
Best Local Similarity	51.0%;	Pred. No. 3.5e-13;		
Matches 205; Conservative	0;	Mismatches 194;	Indels 3;	Gaps 1

QY	245	TTTGTCAGCAACAAAGACAGAACAGATCCCACTAAACAAGACTTATGGCTGTGGCCGCA	304
Db	282	TTGTCAGGCCAATACACTTCTCATGTGCATCAAGACCCATGTTTCTTCACTGCTCTTA	341
QY	305	AAACTGCAATTGGAGTTGAAATTAATGTTTTTATTTTCTGAATACCAAGTAACGTGAC	364
Db	342	GGACTGGGTTGGCTACCAAGAGAAATGCTACTTATTTTCTACTGTAAGAGAGAGCTGAC	401
QY	365	ATTGCCCCAGGCGCTTCTGCATGGCAACAAGGCCCACTAGTCGGTTTGACACACAGAA	424
Db	402	TTCAAGCCAAAATGCTTGTTCTGAAACATGCTCTACTCTGTGTCATTTGATTCTGAAAA	461
QY	425	TGAGCTGAATTTCTTAATGAGATTACAGGCGAATTTTGTATTCCTGGAATGGCCCTGCACAG	484
Db	462	GGACATGAACTTTCTTAAACGATACGAGGTAGAGGGAACACTGGGTGGACTG--AA	518
QY	485	AGAGTGTGTAAGACACCTTTGGAATGGACACACAACTAGTGTATTAACAACAGATTCC	544
Db	519	AAAGGAACCTGGATCACCCATGGAAATGGTCAATATGGCAAGAAATTTAAACAATCTGGTTCAA	578
QY	545	CATCCGGGGAGAGAAAGATTGGCTCACTCTGAACAACAACGGGATCAGCAGTACCCAGAT	604

GenCore version 5.1.8
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OM nucleic - protein search using frame n2p model

Run on: May 23, 2006, 15:44:38 ; Search time 44.5 Seconds
(without alignments) 3717.324 Million cell updates/sec

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Perfect score: 2160
Sequence: 1 gtcctctcagcttcacg.....aataaaccataactac 1206

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 5179358

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blomum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pro -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=LOCAL
-USER=US10031902.OCEN.1.1.364@runat.23052006.145339.461 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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3: geneseqp2000s: *
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6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *
10: geneseqp2006s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1125	52.1	207	4	AAB68583	Aab68583 Murine mo
2	1125	52.1	207	4	ADJ58739	Adj58739 Mouse DCA
3	861.5	39.9	281	8	ADJ67063	Adj67063 Mouse can
4	799	37.0	218	4	AAB68584	Aab68584 Murine mo
5	725	33.6	217	4	AAB68585	Aab68585 Murine mo
6	377	17.5	191	4	AAB68586	Aab68586 Human hOC
7	376	17.4	191	7	ADJ67552	Adj67552 Human Ly1
8	376	17.4	191	8	ADJ93621	Adj93621 Human lec

9	376	17.4	191	8	ADJ58738	Adj58738 Human DCA
10	376	17.4	191	8	ADP12932	Adp12932 Protein e
11	376	17.4	191	8	ADO20149	Ado20149 Human PRO
12	376	17.4	191	8	ADR06494	Adr06494 Human LIT
13	376	17.4	191	8	ADR67078	Adr67078 Human can
14	376	17.4	191	9	ADY17710	Ady17710 PRO polyP
15	376	17.4	191	9	ADY19968	Ady19968 PRO polyP
16	376	17.4	191	10	ABE11652	Abe11652 Human lec
17	376	17.4	191	10	ABE89840	Abe89840 Human LIT
18	376	17.4	191	10	AEF25546	Aef25546 Human lec
19	376	17.4	272	3	AAV94741	Aav94741 Human clo
20	373.5	17.3	181	2	AAW27288	Aaw27288 Human G52
21	373.5	17.3	181	7	ADC36664	Adc36664 Human sec
22	368.5	17.1	149	7	ADF17049	Adf17049 Human alb
23	368.5	17.1	149	8	ADR67070	Adr67070 Human can
24	359	16.6	184	5	ADRA4427	Adra4427 Human CD-
25	351.5	16.3	739	7	ADF17045	Adf17045 Human alb
26	347	16.1	328	3	AAV94744	Aav94744 Murine CD
27	345.5	16.0	132	10	ABE89842	Abe89842 Human LIT
28	345.5	16.0	154	8	AEF25548	Aef25548 Human LIT
29	345.5	16.0	137	4	ADO21118	Ado21118 Human car
30	342.5	15.9	137	4	AAB68578	Aab68578 Murine mo
31	338.5	15.7	132	8	ADJ93623	Adj93623 C-termina
32	317	14.7	288	3	AAV94740	Aav94740 Human clo
33	304	14.1	188	9	AEA89021	Aea89021 Chicken M
34	293.5	13.6	187	5	ADRA4551	Adra4551 Human CD-
35	292	13.5	257	2	AAW85594	Aaw85594 Chicken c-1
36	291	13.5	194	3	AAV94739	Aav94739 Human c-1
37	291	13.5	194	4	AAB74702	Aab74702 Human mem
38	291	13.5	199	2	AAW54659	Aaw54659 Human CD6
39	291	13.5	199	2	AAW85593	Aaw85593 Human CD6
40	291	13.5	199	7	ADJ25621	Adj25621 Binding d
41	291	13.5	199	8	ADJ58741	Adj58741 Human DCA
42	291	13.5	199	8	ADL82855	Adl82855 Human PRO
43	291	13.5	199	8	ADP12478	Adp12478 Protein e
44	291	13.5	199	8	ADP12916	Adp12916 Protein e
45	291	13.5	199	8	ADO19736	Ado19736 Human PRO

ALIGNMENTS

RESULT 1	
AAB68583	standard; protein; 207 AA.
ID	AAB68583
AC	AAB68583;
XX	
DT	25-APR-2001 (first entry)
XX	
DE	Murine mOCIL.
XX	
KW	Osteopathic; mononuclear osteoclast precursor formation inhibition;
KW	calcitonin; osteoclast inhibitory lectin; OCIL; osteoblast; osteoporosis;
KW	osteoclast differentiation; bone resorption; primary hyperparathyroidism;
KW	Paget's disease; rheumatoid arthritis; renal osteodystrophy; murine;
KW	humoral hypercalcaemia; cancer.
XX	
OS	Mus musculus.
XX	
PN	W0200105964-A1.
XX	
PD	25-JAN-2001.
XX	
PF	19-JUL-2000; 2000MO-AU000864.
XX	
PR	19-JUL-1999; 99AU-00001675.
PA	(SVIN-) ST VINCENTS INST MEDICAL RES.
XX	
PI	Zhou H, Kartsoyannis V, Hu Y, Gillespie MT, Ng KW;
XX	
DR	WPI; 2001-103148/11.
XX	

PT Osteoclast inhibitory lectin nucleic acids and polypeptides are expressed
 PT on an osteoblast cell surface and used for treating excessive bone
 PT resorption in conditions such as osteoporosis and Paget's disease.
 XX
 XX Disclosure, Fig 8, 131pp, English.

CC The present invention relates to osteoclast inhibitory lectin coding
 CC sequences and proteins (OCIL). OCIL is a type II membrane protein which
 CC is expressed on osteoblast cell surfaces. OCIL inhibits osteoclast
 CC differentiation from haematopoietic cell precursors. OCIL is useful for
 CC treating a condition with excessive bone resorption, including
 CC osteoporosis, primary hyperparathyroidism, Paget's disease, rheumatoid
 CC arthritis, renal osteodystrophy, humoral hypercalcaemia of malignancy and
 CC conditions where cancer has metastasised to the bone

XX
 SQ Sequence 207 AA;

Alignment Scores:

Pred. No.:	1.02e-102	Length:	207
Score:	1125.00	Matches:	207
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	52.1%	Indels:	0
DB:	4	Gaps:	0

US-10-031-902A-36 (1-1206) x AAB68583 (1-207)

QY 60 ATGTGTGTCAAAAGGCTTCCCTACTATGCTTAGTCCACAGAGCCCGGAGAGGTA 119

DB 1 MetCysValThrIysAlaSerLeuProMetLeuSerProThrIlyserProGIngluVal 20

QY 120 GAAGTGGTAAATTTCTCCAGGAAAAGGACGAGAACCATCTCCCTGAGTGTGCT 179

DB 21 GluValGlyLysIleuGInglYlsArgHsGlyThrIleSerProGInserCysAla 40

QY 180 AAGCTTACTGTACTATGAGATGATCATGTCCTCACTAGCTGTAATTCCTTTCT 239

DB 41 LysIleuTyCysIlyrIrglyValIleMetValIleuThrValAlaValIleAlaLeuSer 60

QY 240 GTTGTCTTTGTACAGCAAAAGACAGACAGATCCCACTCAACAGACTTAGCTGCTTC 239

DB 61 ValAlaLeuSerAlaThrIystrIrgInglIleProValAsnIystrIyAlaAlaCys 80

QY 300 CCGCAAACTGATGATGAGTGAATAATGTTTTATTTCTGTAATCCCAAGTAAC 359

DB 81 ProGInAsnTrpIleGlyValIleAsnIyScyPheTyIryPheSerGInIyTrProSerAsn 100

QY 360 TGGACATTCGCCCGGAGGCTTCTGCATGCGCAAGAGGCCCACTAGCTCGGTTGACAC 419

DB 101 TrpThrPheAlaGlnAlaPheCysMeValIleGIngluAlaGlnIleuAlaArgPheAspAsn 120

QY 420 CAGGATGAGCTGAATTTCTTAATGAGATACAAAGCCAAATTTGATTCCTGGATTGGCCTG 479

DB 121 GlnAspGlnIleuAsnPheLeuMetArgIyIyAlaAsnIheAspSerTrpIleGlyLeu 140

QY 480 CACAGAGAGTCCGACAGACACCTTGGAGTGGACAGACACTGAGTAAACAACAG 539

DB 141 HisArgIleuSerIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleuIleu 160

QY 540 ATTCCCATCCGGGAGAGAAAGATTGCTTACTTGAACAACAACGGGATCAGACAGTACC 599

DB 161 IleProIleArgIleGlyIleuArgPheAlaIleTyLeuAsnIheAsnIleuIleuIleuIleu 180

QY 600 AGGATCTATTCACTTGGATGTGGATGTGAGCAAGCTCAACAGCTTAGCTTCACATGC 659

DB 181 ArgIleTyIserIleuArgMetTrpIleCysIerIyLeuAsnIserIyIserIleuHisCys 200

QY 660 CAACACTCTTTTCTTCTTCC 680

DB 201 GlnThrProPhePheProSer 207

RESULT 2
 ADJ58739

ID ADJ58739 standard; protein; 207 AA.

XX ADJ58739;

XX 06-MAY-2004 (first entry)

XX Mouse DCAL-Hy protein carbohydrate recognition domain (CRD) #1.

XX Type II C-type lectin-like homologue; DCAL-Hy protein; medication;

XX B-cell neoplasm; cancer; drug screening; vaccine; gene therapy;

XX cytoelastic; mouse.

XX Mus musculus.

XX US2004005592-A1.

XX 08-JUN-2004.

XX 03-MAR-2003; 2003US-00379127.

XX 05-MAR-2001; 2001US-00799451.

XX (EMTA/) EMTAGE P C R.

XX (DRMA/) DRMANAC R T.

XX (GOOD/) GOODRICH R W.

XX (TANG/) TANG Y T.

XX Emtage PCR, Drmanac RT, Goodrich RW, Tang YT;

XX WPI; 2004-167523/16.

XX New human DCAL-Hy polypeptides and encoding nucleic acid molecules,

XX useful for diagnosing, preventing or treating B-cell neoplasm (e.g.

XX lymphoma) and in research applications or in drug screening assays.

XX Disclosure; SEQ ID NO 24; 87pp; English.

XX The present invention relates to novel type II C-type lectin-like

XX homologues, including variants, denoted herein as DCAL-Hy 1-5 and

XX collectively known as DCAL-Hy proteins and polynucleotides encoding such

XX proteins. The nucleic acid molecules, polypeptides, anti-DCAL-Hy

XX antibodies or antigen-presenting cells are useful in preparing a

XX medicament or vaccine for killing or inhibiting the growth of DCAL-Hy-

XX expressing cells that cause B-cell neoplasm. The polynucleotides and

XX polypeptides may also be used in diagnosing or preventing cancer, in

XX research applications or in drug screening assays. They are used as

XX vaccines and in gene therapy. The present sequence is mouse DCAL-Hy

XX protein carbohydrate recognition domain (CRD) domain.

XX Sequence 207 AA;

XX Alignment Scores:

Pred. No.:	1.02e-102	Length:	207
Score:	1125.00	Matches:	207
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	52.1%	Indels:	0
DB:	8	Gaps:	0

US-10-031-902A-36 (1-1206) x ADJ58739 (1-207)

QY 60 ATGTGTGTCAAAAGGCTTCCCTACTATGCTTAGTCCACAGAGCCCGGAGAGGTA 119

DB 1 MetCysValThrIysAlaSerLeuProMetLeuSerProThrIlyserProGIngluVal 20

QY 120 GAAGTGGTAAATTTCTCCAGGAAAAGGACGAGAACCATCTCCCTGAGTGTGCT 179

DB 21 GluValGlyLysIleuGInglYlsArgHsGlyThrIleSerProGInserCysAla 40

QY 180 AAGCTTACTGTACTATGAGATGATCATGTCCTCACTAGCTGTAATTCCTTTCT 239

DB 41 LysIleuTyCysIlyrIrglyValIleMetValIleuThrValAlaValIleAlaLeuSer 60

Db 24 Prc

[illegible]


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QY 327 AAATGTTTTTATTTTTCGAATACCCAGTAAGTGGACATTTGGCCAGGCTTTGCATG 386
DB 40 LysCysTyrTyrPheSerGlnSprGluSerAsnTrpHisSerSerGlnHisnEncySsr 59
QY 387 GCACAGAGAGCCCACTAGCTCGTTTGAACAACAGATGAGCTGAATTTCTTATGAGA 446
DB 60 AlaLeuGlyAlaSerIleuAlaValPheAspSerAlaGluAspLeuSerPheThrMetCys 79
QY 447 TACAAAGGCAATTTTATTCCTTGATTTGGCTTGCACAGAGCTGTCAGAGCACCTTGG 506
DB 80 HisLysGlySerSerProHisTrpValGlyLeuSerArgGluGlyLysGlnHisProTyr 99
QY 507 AAGTGACAGACAACTAGTATTAACAACACAGATTCCTCCACTGCCAACTCTTTTCTTCTTGCAT 566
DB 100 GluTrpValAsnArgSerProLeuSerHisLeuPheGlnValGlnIleArgGlyLeuCys 119
QY 567 GCCTTACCTGAACAACAACGAGATCAGACATGACAGATCTTATTCACCTTGGATGGATC 626
DB 120 AlaTyrLeuGlyAspAlaGlyLeuSerSerSerHisCysSerThrArgGlnTrpVal 139
QY 627 TGTAGGAAGCTCAACAGCTATAGCTTCCACTGCCAACTCTTTTCTTCTTGCAT 686
DB 140 CysThrLys-----ProAlaLeuGln 146
QY 687 TTACCAAGAGAGCGCTTTT 704
DB 147 LysProArgLysAsnPhe 152

RESULT 2
150146
gene 17.5 protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50146
R:Bernot, A.; Zoorob, R.; Aufrey, C.
Immunogenetics 39, 221-229, 1994
A:Title: Linkage of a new member of the lectin supergene family to the chicken Mhc genes
A:Reference number: I50146; MIMD:94154691; PMID:8119728
A:Accession: I50146
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-257 <DB>
A:Cross-references: UNIPROT:Q90636; UNIPARC:UPI00000F814E; GB:M88072; NID:G505324; PIDN:
F:129-241/Domain: C-type lectin homology <LCH>

Alignment Scores:
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Score: 292.00 Matches: 65
Percent Similarity: 54.6% Conservative: 36
Best Local Similarity: 35.1% Mismatches: 71
Query Match: 13.5% Indels: 13
DB: 2 Gaps: 5

US-10-031-902A-36 (1-1206) x I50146 (1-257)
QY 101 AGGACAGCCGACAGAGGTAGTAAGTGGTAAATTTCTCAAGGAAAAAGCAGGAAACCAT 160
DB 74 ArgGlnSerGlnArgGly--SerGlyCysSerGlnLeuArgGlnAsnArgGlnArgGly-- 91
QY 161 CTCCTCGAGCTTGTGCTAGCTTACTCTACTACTAGTAGAGTGCATGCTCTCACTGT 220
DB 92 -----ValLeuGlyValAlaLeuSerAlaVal-ProCysMetLeuValLeu----- 106
QY 221 AGCTGAATATGCTCTTCTGTGCTTTGTGACAAACAAGACAGAACAGATCCCACTCAA 280
DB 107 -AlaLeuValAlaValIleValLeuGlnArgProSerCysSerProArgProProPheSe 126
QY 281 CAAGACTATGCTGCTTGGCCGCAAAACGTGATTTGAGATTGAATAATAGTTTATTTT 340
DB 126 rHis-----ValCysProAsnAlaTrpValGlyPheGlnIleLysCysTyrTyrPh 143
QY 341 TTCTGAATACCAAGTAAGTGAACATTCGCCAGGCGCTTGCATGACACAGAGGCCCA 400

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DB 143 eSerPheTrpGlnLysSerZerAspTrpAsnSerSerArgGlnHisCysHisArgLeuGlyAlaSe 163
QY 401 ACTAGTCGGTTTGAACAACAGATGAGCTGAATTTCTTAAAGATACAGAGCGAAATTT 460
DB 163 rLeuAlaThrLeuAspThrLysGlnIleGluTrpLeuGlnIleGluTrpLeuGlnIleGlnArgProAl 183
QY 461 TGATTCCTGATTTGGCTTGCACAGAGAGTCTGACAGACACCTTGGAAATGAGACAGACA 520
DB 183 aAspArgTrpIleGlyLeuHisArgAlaGluIleArgGlnHisTrpThrTrpAlaAspAl 203
QY 521 CACTAGATTAACAAC-----ACGATTCCTATCCGGGAGAGAGAAAGATTGGCTTACCT 574
DB 203 ySerAlaPheThrAsnArgProValPheGluLeuArgGlyGlyArgCysHisLysPheTrpValCysSerAr 223
QY 575 GAACAACAACGGGATGACAGATGACAGATCTTATTCACCTGCGATGCTGATGACAA 634
DB 223 uAsnGlyAspGlyLysSerSerAlaLeuCysHisSerGlnLysPheTrpValCysSerAr 243
QY 635 GCTCAACAGCTAT 647
DB 243 gAlaAspSerTyr 247

RESULT 3
JH0822
Lymphocyte early activation antigen AIM/CD69 - human
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004
C:Accession: JH0822; I56167; S60753
R:Lopez-Cabreira, M.; Santis, A.G.; Fernandez-Ruiz, E.; Blacher, R.; Esch, F.; Sanchez-M
J. Exp. Med. 178, 537-547, 1993
A:Title: Molecular cloning, expression, and chromosomal localization of the human earli
militating receptors.
A:Reference number: JH0822; MIMD:93340630; PMID:8340758
A:Accession: JH0822
A:Molecule type: mRNA
A:Residues: 1-199 <DB>
A:Cross-references: UNIPROT:Q07108; UNIPARC:UPI00000622D7; GB:222576; NID:G397938; PIDN
A:Note: the authors translated the codon CAA for residue 110 as Glu
R:Hamann, J.; Fiebig, H.; Strause, M.
J. Immunol. 150, 4920-4927, 1993
A:Title: Expression cloning of the early activation antigen CD69, a type II integral mem
A:Reference number: I56167; MIMD:93267093; PMID:8496594
A:Accession: I56167
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-199 <RES>
A:Cross-references: UNIPARC:UPI00000622D7; GB:L07555; NID:G291897; PIDN:AA846359.1; PID
R:Santis, A.G.; Lopez-Cabreira, M.; Hamann, J.; Strauss, M.; Sanchez-Madrid, F.
Eur. J. Immunol. 24, 1692-1697, 1994
A:Title: Structure of the gene coding for the human early lymphocyte activation antigen
ceptors.
A:Reference number: S60753; MIMD:94298875; PMID:8026529
A:Accession: S60753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-199 <SAN>
A:Cross-references: UNIPARC:UPI00000622D7; EMBL:Z30426; NID:G525242; PIDN:CAA83017.1; P
C:Comment: This protein is the earliest inducible cell surface glycoprotein expressed in
C:Gene: GDB:CD69
A:Gene: GDB:CD69
A:Cross-references: GDB:132925; OMIM:107273
A:Map position: 12p13-12p12
C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein
F:33-64/Domain: transmembrane #status predicted <TM>
F:85-194/Domain: C-type lectin homology <LCH>
F:18,30/Binding site: phosphate (Ser) (covalent) (by casein kinase C) #status predicted
F:31/Binding site: phosphate (Thr) (covalent) (by casein kinase II) #status predicted
F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 4.05e-20 Length: 199
Score: 291.00 Matches: 62

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GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 23, 2006, 15:44:52 ; Search time 78.8 Seconds
(without alignments)
4247.089 Million cell updates/sec

Title: US-10-031-902A-36

Perfect score: 2160
Sequence: 1 gggccctcgcgttcacgtf.....aaataaaccaataactactac 1206

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 5699196

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-DB=UniProt -QFMT=faetan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORH=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -HOST=abss02p
-USER=US10031902.@CGN.1.1.612.@runcat.23052006.145344.521 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

UniProt_7.2:.*
1: uniProt_sprot:.*
2: uniProt_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1125	52.1	207	2	Q91V08 MOUSE
2	798	36.9	142	2	Q8V119 MOUSE
3	792.5	36.7	269	2	Q9D676 MOUSE
4	787	36.4	207	2	Q3UUY2 MOUSE
5	783	36.2	207	2	Q8BH66 MOUSE
6	775	33.6	202	2	Q924B1 MOUSE
7	725	33.4	217	2	Q9WVF9 MOUSE
8	722	33.4	206	2	Q7TSP7 MOUSE
9	722	33.0	221	2	Q8BFR3 MOUSE
10	712	33.0	158	2	Q80Z35 MOUSE
11	672.5	31.1	186	2	Q8V121 MOUSE
12	650	30.1	156	2	Q7TSP6 MOUSE
13	592.5	27.4	233	2	Q925N7 RAT
14	586.5	27.2	235	2	Q5M911 RAT
15	561	26.0	204	2	Q80XD9 MOUSE
16	539	25.0	204	2	Q8V118 MOUSE

17	516	23.9	206	2	Q924B2 MOUSE	Q924B2 mus musculu
18	516	23.9	218	2	Q8C1T8 MOUSE	Q8C1T8 mus musculu
19	507.5	23.5	180	2	Q9DLS8_YBETA	Q9DLS8 murid herpe
20	376	17.4	191	2	Q9UHP7_HUMAN	Q9UHP7 homo sapien
21	345.5	16.0	133	2	Q6YID5_HUMAN	Q6YID5 homo sapien
22	304	14.1	188	2	Q6ZYD3_CHICK	Q6ZYD3 gallus galli
23	300.5	13.9	200	2	Q802S8_CHICK	Q802S8 gallus galli
24	296	13.7	188	2	Q6ZYD6_CHICK	Q6ZYD6 gallus galli
25	292	13.5	257	2	Q90636_CHICK	Q90636 gallus galli
26	291	13.5	199	1	CD69_HUMAN	Q07108 homo sapien
27	291	13.5	199	1	Q53ZX0_HUMAN	Q53ZX0 homo sapien
28	290.5	13.4	173	2	Q9HD37_HUMAN	Q9HD37 homo sapien
29	285.5	13.2	154	2	Q8WUP7_HUMAN	Q8WUP7 homo sapien
30	282	13.1	149	1	CLC2B_HUMAN	Q8WUP7 homo sapien
31	279	12.9	85	2	Q5RF47_PONPY	Q92478 homo sapien
32	276.5	12.8	200	2	Q8SPX1_PIG	Q8SPX1 sus scrofa
33	274	12.7	52	2	Q8V120_MOUSE	Q8V120 mus musculu
34	268.5	12.4	156	2	Q76LK0_COTJA	Q76LK0 coturnix co
35	258.5	12.0	199	2	Q95M01_BOVIN	Q95M01 bos taurus
36	245.5	11.4	160	2	Q6UWV9_HUMAN	Q6UWV9 homo sapien
37	243	11.2	159	2	Q5M851_RAT	Q5M851 rattus norv
38	242	11.2	199	2	Q5M851_RAT	Q5M851 rattus norv
39	230.5	10.7	141	2	Q6S008_ADEG1	Q6S008 avian adeno
40	228.5	10.6	163	1	V239_F06PV	P14371 fowlpox vir
41	223	10.3	199	1	CD63_MOUSE	P37217 mus musculu
42	223	10.3	199	2	Q3U6A8_MOUSE	Q3U6A8 m bone matr
43	221.5	10.3	132	2	Q8R4K5_RAT	Q8R4K5 rattus norv
44	207	9.6	223	2	Q497F5_MOUSE	Q497F5 mus musculu
45	203	9.4	223	2	Q925G5_MOUSE	Q925G5 mus musculu

ALIGNMENTS

RESULT 1
Q91V08_MOUSE PRELIMINARY; PRT; 207 AA.
AC Q91V08_MOUSE
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 22.
DE C-lectin related CLRB (Osteoclast inhibitory lectin) (C-type lectin domain family 2, member d).
DE domain family 2, member d).
GN Name=Clec2d; Synonyms=Ocll;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX PubMed=14990792; DOI=10.1073/pnas.0308304101;
RA Carlsyle U.R., Jamieson A.M., Gasser S., Clingan C.S., Arase H., Raulet D.H.;
RT "Missing self-recognition of Ocll/Clr-b by inhibitory NKR-P1 natural killer cell receptors.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:3527-3532(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/C; TISSUE=Spleen;
RX PubMed=12126730; PubMed=11278931; DOI=10.1074/jbc.M011554200;
RA Zhou H., Kartsoyianis V., Hu Y.S., Elliott J., Quinn J.M., McKinstrey W.J., Gillespie M.T., Ng K.W.;
RT "A novel osteoclast-derived C-type lectin that inhibits osteoclast formation.";
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6;
RX MEDLINE=2126730; PubMed=11278931; DOI=10.1074/jbc.M011554200;
RA Zhou H., Kartsoyianis V., Hu Y.S., Elliott J., Quinn J.M., McKinstrey W.J., Gillespie M.T., Ng K.W.;
RT "A novel osteoclast-derived C-type lectin that inhibits osteoclast formation.";

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RL J. Biol. Chem. 276:14916-14923(2001).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=129/Sv;
RX MEDLINE=22359051; PubMed=12374791; DOI=10.1074/jbc.M209059200;
RA Zha H., Kartsoyan V., Quinn J.M.W., Ly C., Gange C., Elliott J.,
  Ng K.W., Gillespie M.T.;
RT "osteoclast inhibitory lectin, a family of new osteoclast
  inhibitors.";
  (J. Biol. Chem. 277:48808-48815(2002)).
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
  Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
  Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
  Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
  Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
  Fahy J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
  Rodriguez Y.S.N., Krzywinski M.I., Skalek U., Smaluk D.E.,
  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
  and mouse cDNA sequences.";
  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=PCR rescued clones;
RG NIH MGC Project;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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DR EMBL; AY320031; AAQ16529.1; -; mRNA.
DR EMBL; AF321553; AAK50881.1; -; mRNA.
DR EMBL; AY137338; AAN15947.1; -; Genomic_DNA.
DR EMBL; BC106776; AA106777.1; -; mRNA.
DR HSSP; Q07108; 1FMS.
DR Ensemble; ENSMUSG0000030157; Mus musculus.
DR MGI; MGI:213589; Clec2d.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0046703; F:natural killer cell lectin-like receptor bi. .; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0016066; P:cellular defense response (sensu Vertebrata); TAS.
DR GO; GO:0045671; P:negative regulation of osteoclast different. .; IDA.
DR GO; GO:0042270; P:protection from natural killer cell mediate. .; IDA.
DR InterPro; IPR002353; AntifreezeZell.
DR InterPro; IPR001304; Lectin_C.
DR Pfam; PF00059; Lectin C; 1.
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KW

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DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 19.
DE C lectin-related protein B (Fragment).
GN Name=Ocl; Synonyms=Clec2d;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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OX NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J;
RA Plogasfel B.F.M., Yokoyama W.M.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs License
CC -----
DR EMBL; AF320599; AA137199.1; -; Genomic_DNA.
DR HSSP; Q07108; 1FMS.

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GenCore version 5.1.8
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OM nucleic - protein search, using frame_plus.n2p model

Run on: May 23, 2006, 16:09:18 ; Search time 1.2 Seconds
(without alignments)
644.040 Million cell updates/sec

Title: US-10-031-902a-36

Perfect score: 2160

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 21570 segs, 2136119 residues

Total number of hits satisfying chosen parameters: 43140

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications AA New:

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8: /EMC_Celerra_SIDS3/prodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	376	17.4	191	6	US-10-511-937-2941
2	291	13.5	199	6	US-10-511-937-2487
3	291	13.5	199	6	US-10-511-937-2925
4	217	10.0	100	6	US-10-196-749-578
5	167	7.7	223	6	US-10-511-937-2414
6	159	7.4	201	6	US-10-196-749-108
7	157.5	7.3	190	7	US-11-268-890-4
8	155.5	7.2	376	6	US-10-505-928-77
9	151.5	7.0	231	6	US-10-511-937-2491

10	140	6.5	1456	6	US-10-505-928-69	Sequence 69, App1
11	138.5	6.4	219	6	US-10-196-749-24	Sequence 24, App1
12	129	6.0	188	7	US-11-268-890-2	Sequence 2, App1
13	126.5	5.9	1722	6	US-10-505-928-780	Sequence 780, App1
14	125	5.8	280	6	US-10-196-749-602	Sequence 602, App
15	121.5	5.6	232	6	US-10-196-749-594	Sequence 594, App
16	117.5	5.4	3396	6	US-10-505-928-449	Sequence 449, App
17	114.5	5.3	359	6	US-10-511-937-2932	Sequence 2932, App
18	114.5	5.3	359	6	US-10-511-937-2935	Sequence 2935, App
19	98.5	4.6	830	6	US-10-505-928-469	Sequence 469, App
20	90.5	4.2	1256	6	US-10-511-937-2975	Sequence 2975, App
21	81	3.8	374	6	US-10-505-928-46	Sequence 46, App1
22	80.5	3.7	1842	6	US-10-511-937-2929	Sequence 2929, App
23	79	3.7	382	6	US-10-196-749-20	Sequence 20, App1
24	77	3.6	474	7	US-11-249-111-104	Sequence 104, App
25	76.5	3.5	273	7	US-11-101-316-168	Sequence 168, App
26	76.5	3.5	1019	6	US-10-511-937-2984	Sequence 2984, App
27	76.5	3.5	1435	6	US-10-196-749-581	Sequence 581, App
28	75	3.5	1300	6	US-10-196-749-269	Sequence 269, App
29	75	3.5	175	6	US-10-196-749-424	Sequence 424, App
30	75	3.5	4440	6	US-10-196-749-525	Sequence 525, App
31	72.5	3.4	4373	7	US-11-118-524-2	Sequence 2, App1
32	72	3.3	575	7	US-11-230-593A-29	Sequence 29, App1
33	72	3.3	1743	6	US-10-196-749-451	Sequence 451, App
34	71.5	3.3	373	7	US-11-312-958-10	Sequence 10, App1
35	71	3.3	350	7	US-11-101-316-8	Sequence 8, App1
36	70.5	3.3	4059	6	US-10-501-834-6	Sequence 6, App1
37	70.5	3.3	365	6	US-10-505-928-148	Sequence 148, App1
38	70.5	3.3	610	6	US-10-505-928-580	Sequence 580, App
39	70	3.2	353	6	US-10-322-836-38	Sequence 38, App1
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41	70	3.2	678	6	US-10-322-836-46	Sequence 46, App1
42	70	3.2	633	6	US-10-322-836-34	Sequence 34, App1
43	69.5	3.2	441	6	US-10-511-937-2427	Sequence 2427, App
44	69	3.2	302	7	US-11-181-115-3	Sequence 3, App1
45	69	3.2	562	6	US-10-505-928-547	Sequence 547, App

ALIGNMENTS

RESULT 1
US-10-511-937-2941
; Sequence 2941, Application US/10511937
; Publication No. US200608836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 50661200104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,931
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2941
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2941
Alignment Scores:

Pred. No.: 2,44e-29 Length: 191
Score: 376.00 Matches: 78
Percent Similarity: 57.2% Conservative: 25
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Query Match: 17.4% Indels: 8
DB: 6 Gaps: 4

US-10-031-902a-36 (1-1206) x US-10-511-937-2941 (1-191)

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DB 147 AsnGlyThrGluTrpThrArgGlnPheProIleLeuGlyAlaGlyLysValaIleGlyLeu 166
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RESULT 2

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; Sequence 2487, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 3117
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2487
; LENGTH: 199

TYPE: PRF
ORGANISM: Homo sapiens
US-10-511-937-2487

Alignment Scores: 3,79e-21 Length: 199
Score: 291.00 Matches: 62
Percent Similarity: 49.0% Conservative: 36
Best Local Similarity: 31.0% Mismatches: 94
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DB: 6 Gaps: 5

US-10-031-902a-36 (1-1206) x US-10-511-937-2487 (1-199)

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DB 40 ProValLeuCyAlaValMetAsnValValPhe-----IleThrIleLeuIleIleAla 57
OY 225 GTAATTGCTCTTGTGCTGCT-----TTGTCAAGCAAAAGCAAGACAGATCCCA 275
DB 58 LeuIleAlaLeuSerValGlyGlnTrpAsnCysProGlyGlnTrpThrPheSerMetPro 77
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DB 98 PheIleSerThrValLysArgSerTrpTrpHisSerAlaGlnAsnAlaCysSerGlnHisGly 117
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DB 138 ArgGlnGlnHisTrpValGlyLeuLysGlnIuProGly---HisProTrpLysTrpSer 156
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; Sequence 2925, Application US/10511937
; Publication No. US2006008836A1
; GENERAL INFORMATION:
; APPLICANT: EXPRESSION DIAGNOSTICS, INC.
; APPLICANT: Wohlgenuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, Macdonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
; FILE REFERENCE: 506612000104
; CURRENT APPLICATION NUMBER: US/10/511,937
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: PCT/US2003/012946

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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(without alignments)

3166.858 Million cell updates/sec

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Perfect score: 2160
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 1301182

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	291	13.5	199	US-09-949-016-6129	Sequence 6129, Ap
6	291	13.5	199	PCT-US93-10418-2	Sequence 2, Appl1
7	291	13.5	205	US-09-949-016-10299	Sequence 10299, A
8	290.5	13.4	173	US-09-531-056A-4	Sequence 4, Appl1
9	275	12.7	149	US-09-944-807-6	Sequence 6, Appl1
10	262	12.1	331	US-09-531-056A-12	Sequence 12, Appl1
11	255.5	11.8	78	US-09-531-056A-15	Sequence 15, Appl1

12	255.5	11.8	78	2	US-09-531-056A-16	Sequence 16, Appl1
13	250.5	11.6	115	2	US-08-722-126A-8	Sequence 8, Appl1
14	250.5	11.6	115	5	PCT-US95-04258-8	Sequence 8, Appl1
15	223	10.3	199	5	PCT-US93-10418-4	Sequence 4, Appl1
16	195	9.0	79	2	US-09-531-056A-19	Sequence 19, Appl1
17	189.5	8.8	78	2	US-09-531-056A-18	Sequence 18, Appl1
18	182.5	8.4	225	1	US-08-738-462-2	Sequence 2, Appl1
19	182.5	8.4	225	2	US-09-949-002-339	Sequence 339, App
20	182.5	8.4	225	5	PCT-US94-07587-2	Sequence 2, Appl1
21	180	8.3	78	2	US-09-531-056A-20	Sequence 20, Appl1
22	178	8.2	106	2	US-09-531-056A-8	Sequence 8, Appl1
23	178	8.2	187	2	US-09-535-521-17	Sequence 17, Appl1
24	178	8.2	208	2	US-09-535-521-20	Sequence 20, Appl1
25	178	8.2	232	2	US-09-535-521-2	Sequence 2, Appl1
26	178	8.2	232	2	US-09-535-521-5	Sequence 5, Appl1
27	176.5	8.2	316	2	US-09-111-470-4	Sequence 4, Appl1
28	176.5	8.2	316	3	US-09-862-802A-4	Sequence 4, Appl1
29	176.5	8.2	316	3	US-10-829-107-4	Sequence 4, Appl1
30	175.5	8.1	128	2	US-09-535-521-8	Sequence 8, Appl1
31	175.5	8.1	129	2	US-09-535-521-11	Sequence 11, Appl1
32	175.5	8.1	141	2	US-09-535-521-14	Sequence 14, Appl1
33	174.5	8.1	231	1	US-08-690-095-6	Sequence 6, Appl1
34	174.5	8.1	231	1	US-09-113-789-6	Sequence 6, Appl1
35	174.5	8.1	231	2	US-08-543-246B-6	Sequence 6, Appl1
36	174.5	8.1	231	2	US-08-543-246B-23	Sequence 23, Appl1
37	174	8.1	326	2	US-09-787-192-11	Sequence 11, Appl1
38	173.5	8.0	166	2	US-09-949-002-518	Sequence 518, App
39	173.5	8.0	289	2	US-09-862-802A-13	Sequence 13, Appl1
40	173.5	8.0	289	3	US-10-829-107-13	Sequence 13, Appl1
41	173	8.0	273	2	US-09-111-470-10	Sequence 10, Appl1
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43	173	8.0	273	3	US-10-829-107-10	Sequence 10, Appl1
44	173	8.0	232	1	US-08-688-342-4	Sequence 4, Appl1
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ALIGNMENTS

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; Sequence 6, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531, 056A
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 191
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-6

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Conservative: 25
Mismatches: 69
Indels: 8
Gaps: 4

US-10-031-902A-36 (1-1206) x US-09-531-056A-6 (1-191)

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QY

[illegible]

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RESULT 2
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; Sequence 10300, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241, 755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237, 768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231, 498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10300
; LENGTH: 193
; TYPE: prt
; ORGANISM: Human
US-09-949-016-10300

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Alignment scores:	
Pred. No.:	1,34e-33
Score:	376.00
Percent Similarity:	57.2%
Best Local Similarity:	43.3%
Query Match:	17.4%
DBs:	2
	Gaps: 4

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 QY 162 TCCCTGAAGTCTTGCTAGACTTTACTGCTACTATGAGATGATCATGATCTTCACACTGA 221
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QY	222	GCTGAAATGGCTCTCTGCTGCTCTGGTCAGACAACAACA-----GACACGATGCCA	275
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		:::	
QY	396	GGCCAACTAGCTCGGGTTTGACAACAACAGATGAGCTGAATTTCTTATGGAGATCAACAGCG	455
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QY	456	AATTTTGAATCTCTGGATTTGGCTGCGACACAGAGATGCTGCAGAGCACCCCTTGAAGTGGACA	515
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RESULT 3
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; Sequence 13, Application US/09531056A
; Patent No. 6455683
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SC
; TITLE OF INVENTION: PROTEINS
; FILE REFERENCE: DB20 NP
; CURRENT APPLICATION NUMBER: US/09/531,056A
; CURRENT FILING DATE: 2000-03-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patencin version 3.0
; SEQ ID NO 13
;
; LENGTH: 328
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
US-09-531-056A-13

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DB:	2
Length:	328
Matches:	80
Conserves:	23
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Indels:	28
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[illegible]

FUS

GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: May 23, 2006, 16:07:33 ; Search time 44.2 Seconds

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Fgapop 6.0 , Fgapext 7.0
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Searched: 2097797 seqs, 463214858 residues

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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Database :

Published Applications AA Main: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	376	17.4	191	4	US-10-335-009-2
4	376	17.4	191	4	US-10-379-127-23
5	376	17.4	191	4	US-10-388-838-28
6	376	17.4	191	5	US-10-719-993-569
7	376	17.4	191	5	US-10-770-639-6
8	376	17.4	191	5	US-10-501-841-29
9	376	17.4	191	6	US-11-106-399-2
10	373.5	17.3	181	4	US-10-114-893-22
11	368.5	17.1	149	4	US-10-388-838-20

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13	368.5	17.1	149	5	US-10-775-204-2181	Sequence 2181, App
14	351.5	16.3	179	5	US-10-775-204-2171	Sequence 2171, App
15	345.5	16.0	132	6	US-11-106-399-4	Sequence 4, App1
16	338.5	15.7	132	4	US-10-335-009-4	Sequence 4, App1
17	292	13.5	127	4	US-10-179-528-4	Sequence 4, App1
18	291	13.5	134	3	US-09-965-529-8	Sequence 8, App1
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20	291	13.5	134	6	US-11-048-592-8	Sequence 8, App1
21	291	13.5	139	3	US-09-284-320-86	Sequence 86, App1
22	291	13.5	139	4	US-10-207-655-182	Sequence 182, App
23	291	13.5	139	4	US-10-179-528-3	Sequence 3, App1
24	291	13.5	139	4	US-10-379-127-26	Sequence 26, App1
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26	291	13.5	139	6	US-11-106-399-7	Sequence 7, App1
27	290.5	13.4	134	4	US-10-114-893-28	Sequence 28, App1
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30	282	13.1	149	4	US-10-088-859-2	Sequence 2, App1
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32	275	12.7	149	3	US-09-944-807-6	Sequence 6, App1
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38	250	11.6	139	4	US-10-335-009-7	Sequence 7, App1
39	223	10.3	159	4	US-10-179-528-7	Sequence 7, App1
40	217	10.0	100	4	US-10-052-586-578	Sequence 578, App
41	217	10.0	100	4	US-10-174-590-578	Sequence 578, App
42	217	10.0	100	4	US-10-176-558-578	Sequence 578, App
43	217	10.0	100	4	US-10-175-737-578	Sequence 578, App
44	217	10.0	100	4	US-10-174-581-578	Sequence 578, App
45	217	10.0	100	4	US-10-176-483-578	Sequence 578, App

ALIGNMENTS

RESULT 1
US-10-379-127-24
; Sequence 24, Application US/10379127
; Publication No. US20040005592A1
; GENERAL INFORMATION:
; APPLICANT: Emclac, Peter C.R.
; APPLICANT: Dymac, Radoje
; APPLICANT: Goodrich, Ryle
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THERAPY AND DIAGNOSIS USING TP
; FILE REFERENCE: NUVO-01CIP
; CURRENT APPLICATION NUMBER: US/10/379,127
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 207
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-379-127-24

Alignment Scores:

Pred. No.: 3.43e-110
Score: 1125.00
Percent Similarity: 100.0%
Best Local Similarity: 100.0%
Query Match: 52.1%
DB: 4
Length: 207
Matches: 207
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-031-902A-36 (1-1206) x US-10-379-127-24 (1-207)

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QY 120 GAATGGGTAATAATTCCTCCAGAGAAAAGGACGGAACCATCTCCCTGAGTTCGTGCT 179
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QY 180 AAGCTTCTGCTAGTATGAGTATGATCATAGTCCCTGACGTGCTGATTAATGGCTTCT 239
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Db 161 IleProIleArgGlyGlnGlnAlaArgPheAlaTyrrLeuAsnAsnAsnGlyIleSerSerThr 180
QY 600 AGGATCTATTCACCTTCGATGTGTGATCTGTAGCAGAGCTCAACAGCTATAGCTTCACTGC 659
Db 181 ArgIleTyrrSerLeuArgMetTrpIleCysSerLysLeuAsnSerTyrrSerLeuHisCys 200
QY 660 CAAACTCCTTTTTCCTTCCTCC 680
Db 201 GlnThrProPheProSer 207

RESULT 2
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; Sequence 13, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388, 838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 277
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-388-838-13

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Db 217 GlnHisProTrpTyrrPheAspAsnThrGluTyrrAsnAsnMetIleProIleGlnGly 236
QY 555 GAGGAAAGATTTGCTTACCTGAAACAAACGAGATCAGCAGATCAAGATTAATTCATT 614
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QY 615 CGGATGTGATCTGTGACAAAGCTCAACAGCTATAGCTTACCTGACCAAACTCCT 668
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RESULT 3
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; Sequence 2, Application US/10335009
; Publication No. US20040001804A1
; GENERAL INFORMATION:
; APPLICANT: Porunelloor, Mathew A.
; APPLICANT: Boles, Kent S.
; TITLE OF INVENTION: LIT USES THEREOF IN IMMUNE SYSTEM MODULATION
; FILE REFERENCE: 11707.02/469687-7
; CURRENT APPLICATION NUMBER: US/10/335, 009
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/475,365
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 191
; TYPE: PRT
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